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INFORMATION DISCLOSURE STATEMENT BY APPLICANT

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Sheet 1 of 3

Complete if Known	
Application Number	**10/032,281**
Filing Date	**December 21, 2001**
First Named Inventor	**WYRICK, JOHN**
Art Unit	**1637**
Examiner Name	**Horlick, Kenneth R**
Attorney Docket Number	**WTHD-007CIP**

U.S. PATENT DOCUMENTS

Examiner Initials*	Cite No.[1]	Document Number Number-Kind Code[2] (if known)		Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
		US- 7,297,485	**A2**	**11-20-2004**	**Bornarth, et al.**	
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FOREIGN PATENT DOCUMENTS

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INFORMATION DISCLOSURE STATEMENT BY APPLICANT

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Sheet 2 of 3

Complete if Known	
Application Number	**10/032,281**
Filing Date	**December 21, 2001**
First Named Inventor	**WYRICK, JOHN**
Art Unit	**1637**
Examiner Name	**Horlick, Kenneth R**
Attorney Docket Number	**WTHD-007CIP**

NON PATENT LITERATURE DOCUMENTS			
Examiner Initials*	Cite No.[1]	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T[2]
		BARNARD, et al. PCR bias toward the wild-type k-ras and p53 sequences: Implications for PCR detection of mutations and cancer diagnosis. BioTechniques. 1998, vol. 25, no. 4, pp 684-691.	
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		LOCKHART, et al. Genomics, gene expression and DNA arrays. Nature. 2000, vol. 405, pp. 827-836.	
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		SCHWABE, et al. High-copy cDNA amplification of minimal total RNA quantities for gene expression analyses. Molecular Biotechnology. 2000, vol. 14, pp. 165-172.	

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Sheet 3 of 3

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Art Unit	**1637**
Examiner Name	**Horlick, Kenneth R**
Attorney Docket Number	**WTHD-007CIP**

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		SUZUKI, et al. Kinetic bias in estimates of coastal picoplankton community structure obtained by measurements of small-subunit rRNA gene PCR amplicon length heterogeneity. Applied and Environmental Microbiology. 1998, vol. 64, no. 11, pp. 4522-4529.	
		WADENBACK, et al. Comparison of standard exponential and linear techniques to amplify small cDNA samples for microarrays. BMC Genomics. 2005, vol. 6:61.	
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		WARNECKE, et al. Detection and measurement of PCR bias in quantitative methylation analysis of bisulphite-treated DNA. Nucleic Acids Research. 1997, vol. 25, no. 21, pp. 4422-4426	
		WINTZINGERODE, et al. Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiology Reviews. 1997, vol. 21, pp. 213-229.	

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